

500 Rec'd PCT/PTO 10 JAN 2001

(1) Information for SEQIDNO1:

(a) Sequence Characteristics:

- (i) Length : 2761 base pairs
- (ii) Type : Nucleic acid
- (iii) Strandedness : Double

(b) Molecule type : DNA (genomic)

(c) Original Source:

- (i) Organism : *Neisseria meningitidis*
- (ii) Strain : SD, serogroup B (B:15:Pl.16)

09/743674.011001

(2) Information for SEQIDNO2:

(a) Sequence Characteristics:

- (i) Length : 880 amino acids
- (ii) Type : amino acid
- (iii) Topology : linear

(b) Molecule type : protein

(c) Original Source:

- (i) Organism : *Neisseria meningitidis*
- (ii) Strain : SD, serogroup B (B:15:Pl.16)

09743674-011001

(3) Information for SEQIDNO3:

(a) Sequence Characteristics:

- (i) Length : 1647 base pairs
- (ii) Type : Nucleic acid
- (iii) Strandedness : Double

(b) Molecule type : DNA (genomic)

(c) Original Source:

- (i) Organism : *Neisseria meningitidis*
- (ii) Strain : SD, serogroup B (B:15:Pl.16)

09/43674-011001

(4) Information for SEQIDNO4:

(a) Sequence Characteristics:

(i) Length : 548 amino acids

(ii) Type : amino acid

(iii) Topology : linear

(b) Molecule type : protein

(c) Original Source:

(i) Organism : *Neisseria meningitidis*

(ii) Strain : SD, serogroup B (B:15:Pl.16)

T00110" 429EH260

SEQUENCE LISTING

<110> The University of Nottingham

<120> Screening of Neisserial Vaccine Candidates and Vaccines
against Pathogenic Neisseria.

<130> NW/6940INT

<140> PCT/GB99/02205

<141> 1999-07-09

<150> 9814902.4

<151> 1998-07-10

<160> 4

<170> PatentIn Ver. 2.1

<210> 1

<211> 2761

<212> DNA

<213> Neisseria meningitidis

<220>

<221> CDS

<222> (119)..(2761)

<400> 1

gattgatgca aatatgcaca gatgtttttg aaaaaagatg gagatatgtc ataatttcta 60

aaaacggcga atgattgccg tttaaaatgt ggcggcgggc ggtacattca catattaa 118

atg ccc gcc ggc cga ctg ccc cgc cga tgc cgg atg atg aag aaa ttt 166

Met Pro Ala Gly Arg Leu Pro Arg Arg Cys Pro Met Met Thr Lys Phe
1 5 10 15

aca gac tgt acg cgg tca aac cgt att cag cgg cca acc cac agg gga 214

Thr Asp Cys Thr Arg Ser Asn Arg Ile Gln Pro Pro Thr His Arg Gly
20 25 30

tac atc ttg aaa aac aac aga caa atc aaa ctg att gcc gcc tcc gtc 262

Tyr Ile Leu Lys Asn Asn Arg Gln Ile Lys Leu Ile Ala Ala Ser Val
35 40 45

gca gtt gcc gca tcc ttt cag gca cat gct gga ctg gcc gga ctg aat 310

Ala Val Ala Ala Ser Phe Gln Ala His Ala Gly Leu Gly Gly Leu Asn
50 55 60

atc cag tcc aac ctt gac gaa ccc ttt tcc ggc agc att acc gta acc 358
 Ile Gln Ser Asn Leu Asp Glu Pro Phe Ser Gly Ser Ile Thr Val Thr
 65 70 75 80

ggc gaa gaa gcc aaa gcc ctg cta ggc ggc ggc agc gtt acc gtt tcc 406
 Gly Glu Glu Ala Lys Ala Leu Leu Gly Gly Gly Ser Val Thr Val Ser
 85 90 95

gaa aaa ggc ctg acc gcc aaa gtc cac aag ttg ggc gac aaa gcc gtc 454
 Glu Lys Gly Leu Thr Ala Lys Val His Lys Leu Gly Asp Lys Ala Val
 100 105 110

att gcc gtt tct tcc gaa cag gca gtc cgc gat ccc gtc ctg gta ttc 502
 Ile Ala Val Ser Ser Glu Gln Ala Val Arg Asp Pro Val Leu Val Phe
 115 120 125

cgc atc ggc gca ggc gca cag gta cgc gaa tac acc gcc atc ctc gat 550
 Arg Ile Gly Ala Gly Ala Gln Val Arg Glu Tyr Thr Ala Ile Leu Asp
 130 135 140

cct gtc ggc tac tgg ccc aaa acc aaa tct gca ctt tca gac ggc aag 598
 Pro Val Gly Tyr Ser Pro Lys Thr Lys Ser Ala Leu Ser Asp Gly Lys
 145 150 155 160

aca cac cgc aaa acc gct cgg aca gca gag tcc caa gaa aat caa aac 646
 Thr His Arg Lys Thr Ala Pro Thr Ala Glu Ser Gln Glu Asn Gln Asn
 165 170 175

gcc aaa gcc ctc cgc aaa acc gat aaa aaa gac agc gcg aac gca gcc 694
 Ala Lys Ala Leu Arg Lys Thr Asp Lys Lys Asp Ser Ala Asn Ala Ala
 180 185 190

gtc aaa ccg gcg tac aac gcc aaa acc cat acc gtc cgc aaa ggc gaa 742
 Val Lys Pro Ala Tyr Asn Gly Lys Thr His Thr Val Arg Lys Gly Glu
 195 200 205

acg gtc aaa cag att gcc gcc gcc atc cgc ccg aaa cac ctg acg ctc 790
 Thr Val Lys Gln Ile Ala Ala Ala Ile Arg Pro Lys His Leu Thr Leu
 210 215 220

gaa cag gtt gcc gat gcg ctg ctg aag gca aac cca aat gtt tcc gca 838
 Glu Gln Val Ala Asp Ala Leu Leu Lys Ala Asn Pro Asn Val Ser Ala
 225 230 235 240

cac ggc aga ctg cgt gcg gcc agc gtc ctt cac att ccg aat ctg aac 886
 His Gly Arg Leu Arg Ala Gly Ser Val Leu His Ile Pro Asn Leu Asn
 245 250 255

agg atc aaa gcg gaa caa ccc aaa ccg caa acg gcg aaa ccc aaa gcc 934
 Arg Ile Lys Ala Glu Gln Pro Lys Pro Gln Thr Ala Lys Pro Lys Ala
 260 265 270

gaa acc gca tcc atg ccg tcc gaa ccg tcc aaa cag gca acg gta gag 962
 Glu Thr Ala Ser Met Pro Ser Glu Pro Ser Lys Gln Ala Thr Val Glu
 275 280 285

aaa ccg gtt gaa aaa cct gaa gca aaa gtt gcc gcg ccc gaa gca aaa 1030
 Lys Pro Val Glu Lys Pro Glu Ala Lys Val Ala Ala Pro Glu Ala Lys
 290 295 300

gcg gaa aaa ccg gcc gtt cga ccc gaa cct gta ccc gct gca aat act 1078
 Ala Glu Lys Pro Ala Val Arg Pro Glu Pro Val Pro Ala Ala Asn Thr
 305 310 315 320

gcc gca tcc gaa acc gct gcc gaa tcc gcc ccc caa gaa gcc gcc gct 1126
 Ala Ala Ser Glu Thr Ala Ala Glu Ser Ala Pro Gln Glu Ala Ala Ala
 325 330 335

tct gcc atc gac acg ccg acc gac gaa acc ggt aac gcc gtt tcc gaa 1174
 Ser Ala Ile Asp Thr Pro Thr Asp Glu Thr Gly Asn Ala Val Ser Glu
 340 345 350

cct gtc gaa cag gtt tct gcc gaa gaa gaa acc gaa agc gga ctg ttc 1222
 Pro Val Glu Gln Val Ser Ala Glu Glu Glu Thr Glu Ser Gly Leu Phe
 355 360 365

ggc ggt tcc tac acc ttc ctg ctt gcc gcc gga gcc gcg gca ttg atc 1270
 Gly Gly Ser Tyr Thr Leu Leu Ala Gly Gly Ala Ala Ala Leu Ile
 370 375 380

gcc ctg ctg ctg ctt ttg cgc ctt gcc caa tcc aaa cgc gcg gcc cgt 1318
 Ala Leu Leu Leu Leu Leu Arg Leu Ala Gln Ser Lys Arg Ala Arg Arg
 385 390 395 400

acc gaa gaa tcc gtc cct gag gaa gag cct gac ctt gac gac gcg gca 1366
 Thr Glu Glu Ser Val Pro Glu Glu Glu Pro Asp Leu Asp Asp Ala Ala
 405 410 415

gac gac gcc ata gaa atc acc ttt gcc gaa gtc gaa act ccg gca acg 1414
 Asp Asp Gly Ile Glu Ile Thr Phe Ala Glu Val Glu Thr Pro Ala Thr
 420 425 430

ccc gaa ccc gct ccg aaa aac gat gta aac gac aca ctt gcc tta gat 1462
 Pro Glu Pro Ala Pro Lys Asn Asp Val Asn Asp Thr Leu Ala Leu Asp
 435 440 445

ggg gaa tct gaa gaa gag ttg tgg gca aaa caa acg ttc gat gtc gaa 1510
 Gly Glu Ser Glu Glu Glu Leu Ser Ala Lys Gln Thr Phe Asp Val Glu
 450 455 460

acc gat acg cct tcc aac cgc atc gac ttg gat ttc gac agc ctg gca 1558
 Thr Asp Thr Pro Ser Asn Arg Ile Asp Leu Asp Phe Asp Ser Leu Ala
 465 470 475 480

gcc gcg caa aac ggc att tta tcc ggc gca ctt acg cag gat gaa gaa 1606
 Ala Ala Gln Asn Gly Ile Leu Ser Gly Ala Leu Thr Gln Asp Glu Glu
 485 490 495

acc caa aaa cgc gcg gat gcc gat tgg aac gcc atc gaa tcc aca gac 1654
 Thr Gln Lys Arg Ala Asp Ala Asp Trp Asn Ala Ile Glu Ser Thr Asp
 500 505 510

agc gtg tac gag ccc gag acc ttc aac ccg tac aac cct gtc gaa atc 1702
 Ser Val Tyr Glu Pro Glu Thr Phe Asn Pro Tyr Asn Pro Val Glu Ile
 515 520 525

gtc atc gac acg ccc gaa ccg gaa tct gtc gcc caa act gcc gaa aac 1750
 Val Ile Asp Thr Pro Glu Pro Glu Ser Val Ala Gln Thr Ala Glu Asn
 530 535 540

aaa ccg gaa acc gtc gat acc gat ttc tcc gac aac ctg ccc tca aac 1798
 Lys Pro Glu Thr Val Asp Thr Asp Phe Ser Asp Asn Leu Pro Ser Asn
 545 550 555 560

aac cat atc ggc aca gaa gaa aca ggt tcc gca aaa cct gcc tca ccc 1846
 Asn His Ile Gly Thr Glu Glu Thr Ala Ser Ala Lys Pro Ala Ser Pro
 565 570 575

tcc gga ctg gca ggc ttc ctg aag ggt tcc tgg ccc gaa acc atc ttg 1894
 Ser Gly Leu Ala Gly Phe Leu Lys Ala Ser Ser Pro Glu Thr Ile Leu
 580 585 590

gaa aaa aca gtt gcc gaa gtc caa aca ccg gaa gag ttg cac gat ttc 1942
 Glu Lys Thr Val Ala Glu Val Gln Thr Pro Glu Glu Leu His Asp Phe
 595 600 605

ctg aaa gtg tac gaa acc gat gcc gtc gcg gaa act gcg cct gaa acg 1990
 Leu Lys Val Tyr Glu Thr Asp Ala Val Ala Glu Thr Ala Pro Glu Thr
 610 615 620

ccc gat ttc aac gcc gcc gca gac gat ttg tcc gca ttg ctt caa cct 2038
 Pro Asp Phe Asn Ala Ala Ala Asp Asp Leu Ser Ala Leu Leu Gln Pro
 625 630 635 640

gcc gaa gca ccg ttc gtt gag gaa aat ata acg gaa acc gcc gaa 2086
 Ala Glu Ala Pro Ser Val Glu Glu Asn Ile Thr Glu Thr Ala Glu
 645 650 655

aca ccc gac ttc aac gcc acc gca gac gat ttg tcc gca tta ctt caa 2134
 Thr Pro Asp Phe Asn Ala Thr Ala Asp Asp Leu Ser Ala Leu Leu Gln
 660 665 670

cct tct gaa gta cct gcc gtt gag gaa aat gca gcg gaa atc gtt gcc 2182
 Pro Ser Glu Val Pro Ala Val Glu Glu Asn Ala Ala Glu Ile Val Ala
 675 680 685

gat gat ttg tcc gca ctg ttg caa cct gct gaa gca ccg gct gtt gag 2230
 Asp Asp Leu Ser Ala Leu Leu Gln Pro Ala Glu Ala Pro Ala Val Glu
 690 695 700

gaa aat gta acg gaa act gtt gcc gaa acg tcc gac ttc cac acc gcc 2278
 Glu Asn Val Thr Glu Thr Val Ala Glu Thr Ser Asp Phe His Thr Ala
 705 710 715 720

gca gac gat ttg tcc gca ctg ttg caa cct gct gaa gta ccg gcc gtt 2326
 Ala Asp Asp Leu Ser Ala Leu Leu Gln Pro Ala Glu Val Pro Ala Val
 725 730 735

gag gaa aat gta acg aaa acc gtt gcc gaa ata cct gat ttc aac gcc 2374
 Glu Glu Asn Val Thr Lys Thr Val Ala Glu Ile Pro Asp Phe Asn Ala
 740 745 750

acc gca gac gat ttg tcc gca tta ctt caa cct tct gaa gta ccg gcc 2422
 Thr Ala Asp Asp Leu Ser Ala Leu Leu Gln Pro Ser Glu Val Pro Ala
 755 760 765

gtt gag gaa aat gca gcg gaa atc act ttg gaa acg cct gat tcc aac 2470
 Val Glu Glu Asn Ala Ala Glu Ile Thr Leu Glu Thr Pro Asp Ser Asn
 770 775 780

acc tct gag gca gac gct ttg ccc gac ttc ctg aaa gac ggc gag gag 2518
 Thr Ser Glu Ala Asp Ala Leu Pro Asp Phe Leu Lys Asp Gly Glu Glu
 785 790 795 800

gaa acg gta gat tgg agc atc tac ctc tcg gaa gaa aat atc cca aat 2566
 Glu Thr Val Asp Trp Ser Ile Tyr Leu Ser Glu Glu Asn Ile Pro Asn
 805 810 815

aat gca gat acc agt ttc cct tcg gaa tct gta ggt tct gac gcg cct 2614
 Asn Ala Asp Thr Ser Phe Pro Ser Glu Ser Val Gly Ser Asp Ala Pro
 820 825 830

00443674 011001

ccc gaa gcg aaa tac gac ctt gcc gaa atg tat ctc gaa atc gcc gac 2662
 Ser Glu Ala Lys Tyr Asp Leu Ala Glu Met Tyr Leu Glu Ile Gly Asp
 835 840 845

cgc gat gcc gct gcc gag aca gtg cag aaa ttg ctg gaa gaa gcc gaa 2710
 Arg Asp Ala Ala Ala Glu Thr Val Gln Lys Leu Leu Glu Glu Ala Glu
 850 855 860

ggc gac gta ctc aaa cgt gcc caa gca ttg gcg cag gaa ttg ggt att 2758
 Gly Asp Val Leu Lys Arg Ala Gln Ala Leu Ala Gln Glu Leu Gly Ile
 865 870 875 880

tga 2761

<210> 2

<211> 880

<212> PRT

<213> Neisseria meningitidis

<400> 2

Met Pro Ala Gly Arg Leu Pro Arg Arg Cys Pro Met Met Thr Lys Phe
 1 5 10 15

Thr Asp Cys Thr Arg Ser Asn Arg Ile Gln Pro Pro Thr His Arg Gly
 20 25 30

Tyr Ile Leu Lys Asn Asn Arg Gln Ile Lys Leu Ile Ala Ala Ser Val
 35 40 45

Ala Val Ala Ala Ser Phe Gln Ala His Ala Gly Leu Gly Gly Leu Asn
 50 55 60

Ile Gln Ser Asn Leu Asp Glu Pro Phe Ser Gly Ser Ile Thr Val Thr
 65 70 75 80

Gly Glu Glu Ala Lys Ala Leu Leu Gly Gly Gly Ser Val Thr Val Ser
 85 90 95

Glu Lys Gly Leu Thr Ala Lys Val His Lys Leu Gly Asp Lys Ala Val
 100 105 110

Ile Ala Val Ser Ser Glu Gln Ala Val Arg Asp Pro Val Leu Val Phe
 115 120 125

Arg Ile Gly Ala Gly Ala Gln Val Arg Glu Tyr Thr Ala Ile Leu Asp

09743674-011001

130

135

140

Pro Val Gly Tyr Ser Pro Lys Thr Lys Ser Ala Leu Ser Asp Gly Lys
145 150 155 160

Thr His Arg Lys Thr Ala Pro Thr Ala Glu Ser Gln Glu Asn Gln Asn
165 170 175

Ala Lys Ala Leu Arg Lys Thr Asp Lys Lys Asp Ser Ala Asn Ala Ala
180 185 190

Val Lys Pro Ala Tyr Asn Gly Lys Thr His Thr Val Arg Lys Gly Glu
195 200 205

Thr Val Lys Gln Ile Ala Ala Ala Ile Arg Pro Lys His Leu Thr Leu
210 215 220

Glu Gln Val Ala Asp Ala Leu Leu Lys Ala Asn Pro Asn Val Ser Ala
225 230 235 240

His Gly Arg Leu Arg Ala Gly Ser Val Leu His Ile Pro Asn Leu Asn
245 250 255

Arg Ile Lys Ala Glu Gln Pro Lys Pro Gln Thr Ala Lys Pro Lys Ala
260 265 270

Glu Thr Ala Ser Met Pro Ser Glu Pro Ser Lys Gln Ala Thr Val Glu
275 280 285

Lys Pro Val Glu Lys Pro Glu Ala Lys Val Ala Ala Pro Glu Ala Lys
290 295 300

Ala Glu Lys Pro Ala Val Arg Pro Glu Pro Val Pro Ala Ala Asn Thr
305 310 315 320

Ala Ala Ser Glu Thr Ala Ala Glu Ser Ala Pro Gln Glu Ala Ala Ala
325 330 335

Ser Ala Ile Asp Thr Pro Thr Asp Glu Thr Gly Asn Ala Val Ser Glu
340 345 350

Pro Val Glu Gln Val Ser Ala Glu Glu Glu Thr Glu Ser Gly Leu Phe
355 360 365

Gly Gly Ser Tyr Thr Leu Leu Leu Ala Gly Gly Gly Ala Ala Leu Ile
370 375 380

Ala Leu Leu Leu Leu Leu Arg Leu Ala Gln Ser Lys Arg Ala Arg Arg

09743674 011001

385 390 395 400
 Thr Glu Glu Ser Val Pro Glu Glu Glu Pro Asp Leu Asp Asp Ala Ala
 405 410 415
 Asp Asp Gly Ile Glu Ile Thr Phe Ala Glu Val Glu Thr Pro Ala Thr
 420 425 430
 Pro Glu Pro Ala Pro Lys Asn Asp Val Asn Asp Thr Leu Ala Leu Asp
 435 440 445
 Gly Glu Ser Glu Glu Glu Leu Ser Ala Lys Gln Thr Phe Asp Val Glu
 450 455 460
 Thr Asp Thr Pro Ser Asn Arg Ile Asp Leu Asp Phe Asp Ser Leu Ala
 465 470 475 480
 Ala Ala Gln Asn Gly Ile Leu Ser Gly Ala Leu Thr Gln Asp Glu Glu
 485 490 495
 Thr Gln Lys Arg Ala Asp Ala Asp Trp Asn Ala Ile Glu Ser Thr Asp
 500 505 510
 Ser Val Tyr Glu Pro Glu Thr Phe Asn Pro Tyr Asn Pro Val Glu Ile
 515 520 525
 Val Ile Asp Thr Pro Glu Pro Glu Ser Val Ala Gln Thr Ala Glu Asn
 530 535 540
 Lys Pro Glu Thr Val Asp Thr Asp Phe Ser Asp Asn Leu Pro Ser Asn
 545 550 555 560
 Asn His Ile Gly Thr Glu Glu Thr Ala Ser Ala Lys Pro Ala Ser Pro
 565 570 575
 Ser Gly Leu Ala Gly Phe Leu Lys Ala Ser Ser Pro Glu Thr Ile Leu
 580 585 590
 Glu Lys Thr Val Ala Glu Val Gln Thr Pro Glu Glu Leu His Asp Phe
 595 600 605
 Leu Lys Val Tyr Glu Thr Asp Ala Val Ala Glu Thr Ala Pro Glu Thr
 610 615 620
 Pro Asp Phe Asn Ala Ala Ala Asp Asp Leu Ser Ala Leu Leu Gln Pro
 625 630 635 640
 Ala Glu Ala Pro Ser Val Glu Glu Asn Ile Thr Glu Thr Val Ala Glu

645

650

655

Thr Pro Asp Phe Asn Ala Thr Ala Asp Asp Leu Ser Ala Leu Leu Gln
660 665 670

Pro Ser Glu Val Pro Ala Val Glu Glu Asn Ala Ala Glu Ile Val Ala
675 680 685

Asp Asp Leu Ser Ala Leu Leu Gln Pro Ala Glu Ala Pro Ala Val Glu
690 695 700

Glu Asn Val Thr Glu Thr Val Ala Glu Thr Ser Asp Phe His Thr Ala
705 710 715 720

Ala Asp Asp Leu Ser Ala Leu Leu Gln Pro Ala Glu Val Pro Ala Val
725 730 735

Glu Glu Asn Val Thr Lys Thr Val Ala Glu Ile Pro Asp Phe Asn Ala
740 745 750

Thr Ala Asp Asp Leu Ser Ala Leu Leu Gln Pro Ser Glu Val Pro Ala
755 760 765

Val Glu Glu Asn Ala Ala Glu Ile Thr Leu Glu Thr Pro Asp Ser Asn
770 775 780

Thr Ser Glu Ala Asp Ala Leu Pro Asp Phe Leu Lys Asp Gly Glu Glu
785 790 795 800

Glu Thr Val Asp Trp Ser Ile Tyr Leu Ser Glu Glu Asn Ile Pro Asn
805 810 815

Asn Ala Asp Thr Ser Phe Pro Ser Glu Ser Val Gly Ser Asp Ala Pro
820 825 830

Ser Glu Ala Lys Tyr Asp Leu Ala Glu Met Tyr Leu Glu Ile Gly Asp
835 840 845

Arg Asp Ala Ala Ala Glu Thr Val Gln Lys Leu Leu Glu Glu Ala Glu
850 855 860

Gly Asp Val Leu Lys Arg Ala Gln Ala Leu Ala Gln Glu Leu Gly Ile
865 870 875 880

<210> 3

<211> 1647

09743674.011001

<212> DNA

<213> Neisseria meningitidis

<220>

<221> CDS

<222> (1)..(1647)

<400> 3

atg aag caa aat gtt atg ttt ctt atc cta ggg cga aat ttt tta aag	48
Met Lys Gln Asn Val Met Phe Leu Ile Leu Gly Arg Asn Phe Leu Lys	
1 5 10 15	
att atc cta tgc ttt agt ttt ttt gta cct aaa ttt gca ttg gca tca	96
Ile Ile Leu Cys Phe Ser Phe Phe Val Pro Lys Phe Ala Leu Ala Ser	
20 25 30	
gta aat gtt cgg ggt aaa ttt gat agg gtt gaa gtt tat gat gat ggc	144
Val Asn Val Pro Gly Lys Phe Asp Arg Val Glu Val Tyr Asp Asp Gly	
35 40 45	
aga tat tta ggt att cga ggt tca gat gac aaa aga aga aga att tgg	192
Arg Tyr Leu Gly Ile Arg Gly Ser Asp Asp Lys Arg Arg Arg Ile Trp	
50 55 60	
aaa ggt gta ttt gat aga gaa tgg gga aga tat tta act tca gaa gct	240
Lys Gly Val Phe Asp Arg Glu Ser Gly Arg Tyr Leu Thr Ser Glu Ala	
65 70 75 80	
caa gat tta aaa gtt agg cat gta tct act gga gca tca agt acg ggt	288
Gln Asp Leu Lys Val Arg His Val Ser Thr Gly Ala Ser Ser Thr Gly	
85 90 95	
aaa gtt agt tgg gtt gta tct tca tca gtt tcc cgc gcc gga gtc ttg	336
Lys Val Ser Ser Val Val Ser Ser Ser Val Ser Arg Ala Gly Val Leu	
100 105 110	
gca gga gtc gcc aaa ctt gcc cgc tta ggc gcg aaa tta agc aca agg	384
Ala Gly Val Gly Lys Leu Ala Arg Leu Gly Ala Lys Leu Ser Thr Arg	
115 120 125	
gca gtt cct tat gtc gga aca gcc ctt tta gcc cat gac gta tac gaa	432
Ala Val Pro Tyr Val Gly Thr Ala Leu Leu Ala His Asp Val Tyr Glu	
130 135 140	
act ttc aaa gaa gac ata cag gca caa ggc tac caa tac gac ccc gaa	480
Thr Phe Lys Glu Asp Ile Gln Ala Gln Gly Tyr Gln Tyr Asp Pro Glu	
145 150 155 160	

acc gac aaa ttt gta aaa ggc tac gaa tat agt aat tgc ctt tgg tac 528
 Thr Asp Lys Phe Val Lys Gly Tyr Glu Tyr Ser Asn Cys Leu Trp Tyr
 165 170 175

gaa gac aaa aga cgt att aat aga acc tat ggc tgc tac ggc gtt gac 576
 Glu Asp Lys Arg Arg Ile Asn Arg Thr Tyr Gly Cys Tyr Gly Val Asp
 180 185 190

agt tcc att arg cgc att atg tcc gat gac agc aga ttc ccc gaa gtc 624
 Ser Ser Ile Met Arg Leu Met Ser Asp Asp Ser Arg Phe Pro Glu Val
 195 200 205

aaa gaa ttg atg gaa agc caa atg tat agg ctg gca cgt ccg ttt tgg 672
 Lys Glu Leu Met Glu Ser Gln Met Tyr Arg Leu Ala Arg Pro Phe Trp
 210 215 220

aat tgg cat aaa gaa gaa ctg aat aaa tta agt tct ttg gat tgg aat 720
 Asn Trp His Lys Glu Glu Leu Asn Lys Leu Ser Ser Leu Asp Trp Asn
 225 230 235 240

aat ttt gtt tta aat cgt tgc aca att aat tgg aat ggc gga gat tgt 768
 Asn Phe Val Leu Asn Arg Cys Thr Phe Asn Trp Asn Gly Gly Asp Cys
 245 250 255

ttg gtc aat aaa ggt gat gat ttc aga aat ggg gct gat ttt tcc ctt 816
 Leu Val Asn Lys Gly Asp Asp Phe Arg Asn Gly Ala Asp Phe Ser Leu
 260 265 270

att cgc aat tca aaa tac aaa gaa gaa atg gat gcc aaa aag ctg gaa 864
 Ile Arg Asn Ser Lys Tyr Lys Glu Glu Met Asp Ala Lys Lys Leu Glu
 275 280 285

gag att tta tcc ttg aaa gtc gat gcc aat ccc gac aaa tac ata aag 912
 Glu Ile Leu Ser Leu Lys Val Asp Ala Asn Pro Asp Lys Tyr Ile Lys
 290 295 300

gaa acc ggt tat ccc ggt tat tcc jaa aaa gta gaa gtc gca ccc gga 960
 Glu Thr Gly Tyr Pro Gly Tyr Ser Glu Lys Val Glu Val Ala Pro Gly
 305 310 315 320

aca aaa gtg aat atg ggt ccc gtc acg gac agg aac ggg aat ccc gtt 1008
 Thr Lys Val Asn Met Gly Pro Val Thr Asp Arg Asn Gly Asn Pro Val
 325 330 335

cag gtt gtc gca aca ttc ggc agg gat tcc caa ggc aac acc acg gtg 1056
 Gln Val Val Ala Thr Phe Gly Arg Asp Ser Gln Gly Asn Thr Thr Val
 340 345 350

09743674-011001

gat gtt caa gta atc ccg cgt ccc gac ttg acc ccc gga agc gcg gaa 1104
 Asp Val Gln Val Ile Pro Arg Pro Asp Leu Thr Pro Gly Ser Ala Glu
 355 360 365

gca cgg aac gca cag ccg ctg ccc gaa gta tcg ccc gcc gaa aac ccc 1152
 Ala Pro Asn Ala Gln Pro Leu Pro Glu Val Ser Pro Ala Glu Asn Pro
 370 375 380

gca aac aac ccg aac ccc aat gag aac ccc ggc acg agc ccc aat ccc 1200
 Ala Asn Asn Pro Asn Pro Asn Glu Asn Pro Gly Thr Ser Pro Asn Pro
 385 390 395 400

gaa ccc gac ccc gat ttg aat ccc gat gca aat ccc gat acg gac gga 1248
 Glu Pro Asp Pro Asp Leu Asn Pro Asp Ala Asn Pro Asp Thr Asp Gly
 405 410 415

cag ccc ggc aca aga ccc gat tcc ccc gcc gtt ccg gga cgc aca aac 1296
 Gln Pro Gly Thr Arg Pro Asp Ser Pro Ala Val Pro Gly Arg Thr Asn
 420 425 430

ggc agg gac gcc aaa gac gga aag gac gcc aaa gat gcc gcc ctt ttg 1344
 Gly Arg Asp Gly Lys Asp Gly Lys Asp Gly Lys Asp Gly Gly Leu Leu
 435 440 445

tgc aaa ttc ttc ccc gac att ctc gct tgc gac agg ctg ccc gag tcc 1392
 Cys Lys Phe Phe Pro Asp Ile Leu Ala Cys Asp Arg Leu Pro Glu Ser
 450 455 460

aat ccg gca gaa gat tta aat ctg ccg tct gaa acc gtc aat gta gag 1440
 Asn Pro Ala Glu Asp Leu Asn Leu Pro Ser Glu Thr Val Asn Val Glu
 465 470 475 480

ttt cag aaa tca gga atc ttt caa gat tcc gca cag tgt ccc gca cct 1488
 Phe Gln Lys Ser Gly Ile Phe Gln Asp Ser Ala Gln Cys Pro Ala Pro
 485 490 495

gtc act ttc aca gtg act gtg ctt gat tca agc agg cag ttc gcg ttc 1536
 Val Thr Phe Thr Val Thr Val Leu Asp Ser Ser Arg Gln Phe Ala Phe
 500 505 510

agc ttt gag aac gca tgt acc ata gcc gaa cgg cta agg tac atg ctt 1584
 Ser Phe Glu Asn Ala Cys Thr Ile Ala Glu Arg Leu Arg Tyr Met Leu
 515 520 525

ctc gcc ctt gct tgg gcg gtt gcc gcc ttt ttt tgt atc cgc aca gta 1632
 Leu Ala Leu Ala Trp Ala Val Ala Ala Phe Phe Cys Ile Arg Thr Val
 530 535 540

09743574-011001

tct cgt gaa gtc tag
 Ser Arg Glu Val
 545

1647

<210> 4
 <211> 548
 <212> FRT
 <213> Neisseria meningitidis

<400> 4
 Met Lys Gln Asn Val Met Phe Leu Ile Leu Gly Arg Asn Phe Leu Lys
 1 5 10 15

Ile Ile Leu Cys Phe Ser Phe Phe Val Pro Lys Phe Ala Leu Ala Ser
 20 25 30

Val Asn Val Pro Gly Lys Phe Asp Arg Val Glu Val Tyr Asp Asp Gly
 35 40 45

Arg Tyr Leu Gly Ile Arg Gly Ser Asp Asp Lys Arg Arg Arg Ile Trp
 50 55 60

Lys Gly Val Phe Asp Arg Glu Ser Gly Arg Tyr Leu Thr Ser Glu Ala
 65 70 75 80

Gln Asp Leu Lys Val Arg His Val Ser Thr Gly Ala Ser Ser Thr Gly
 85 90 95

Lys Val Ser Ser Val Val Ser Ser Ser Val Ser Arg Ala Gly Val Leu
 100 105 110

Ala Gly Val Gly Lys Leu Ala Arg Leu Gly Ala Lys Leu Ser Thr Arg
 115 120 125

Ala Val Pro Tyr Val Gly Thr Ala Leu Leu Ala His Asp Val Tyr Glu
 130 135 140

Thr Phe Lys Glu Asp Ile Gln Ala Gln Gly Tyr Gln Tyr Asp Pro Glu
 145 150 155 160

Thr Asp Lys Phe Val Lys Gly Tyr Glu Tyr Ser Asn Cys Leu Trp Tyr
 165 170 175

Glu Asp Lys Arg Arg Ile Asn Arg Thr Tyr Gly Cys Tyr Gly Val Asp
 180 185 190

Ser Ser Ile Met Arg Leu Met Ser Asp Asp Ser Arg Phe Pro Glu Val

09743674-011001

195

200

205

Lys Glu Leu Met Glu Ser Gln Met Tyr Arg Leu Ala Arg Pro Phe Trp
 210 215 220

Asn Trp His Lys Glu Glu Leu Asn Lys Leu Ser Ser Leu Asp Trp Asn
 225 230 235 240

Asn Phe Val Leu Asn Arg Cys Thr Phe Asn Trp Asn Gly Gly Asp Cys
 245 250 255

Leu Val Asn Lys Gly Asp Asp Phe Arg Asn Gly Ala Asp Phe Ser Leu
 260 265 270

Ile Arg Asn Ser Lys Tyr Lys Glu Glu Met Asp Ala Lys Lys Leu Glu
 275 280 285

Glu Ile Leu Ser Leu Lys Val Asp Ala Asn Pro Asp Lys Tyr Ile Lys
 290 295 300

Glu Thr Gly Tyr Pro Gly Tyr Ser Glu Lys Val Glu Val Ala Pro Gly
 305 310 315 320

Thr Lys Val Asn Met Gly Pro Val Thr Asp Arg Asn Gly Asn Pro Val
 325 330 335

Gln Val Val Ala Thr Phe Gly Arg Asp Ser Gln Gly Asn Thr Thr Val
 340 345 350

Asp Val Gln Val Ile Pro Arg Pro Asp Leu Thr Pro Gly Ser Ala Glu
 355 360 365

Ala Pro Asn Ala Gln Pro Leu Pro Glu Val Ser Pro Ala Glu Asn Pro
 370 375 380

Ala Asn Asn Pro Asn Pro Asn Glu Asn Pro Gly Thr Ser Pro Asn Pro
 385 390 395 400

Glu Pro Asp Pro Asp Leu Asn Pro Asp Ala Asn Pro Asp Thr Asp Gly
 405 410 415

Gln Pro Gly Thr Arg Pro Asp Ser Pro Ala Val Pro Gly Arg Thr Asn
 420 425 430

Gly Arg Asp Gly Lys Asp Gly Lys Asp Gly Lys Asp Gly Gly Leu Leu
 435 440 445

Cys Lys Phe Phe Pro Asp Ile Leu Ala Cys Asp Arg Leu Pro Glu Ser

00743674.011004
 T00770.4267460

450

455

460

Asn Pro Ala Glu Asp Leu Asn Leu Pro Ser Glu Thr Val Asn Val Glu
 465 470 475 480

Phe Gln Lys Ser Gly Ile Phe Gln Asp Ser Ala Gln Cys Pro Ala Pro
 485 490 495

Val Thr Phe Thr Val Thr Val Leu Asp Ser Ser Arg Gln Phe Ala Phe
 500 505 510

Ser Phe Glu Asn Ala Cys Thr Ile Ala Glu Arg Leu Arg Tyr Met Leu
 515 520 525

Leu Ala Leu Ala Trp Ala Val Ala Ala Phe Phe Cys Ile Arg Thr Val
 530 535 540

Ser Arg Glu Val
 545

100710" 1492460